T03030 T6T92650

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NUCLEIC ACID MOLECULES ENCODING TRANSMEMBRANE SERINE PROTEASES, THE ENCODED PROTEINS AND METHODS BASED THEREON
DOCKET NO. 24745-1607
Filed: February 2, 2001

Domain organization of MTSP3

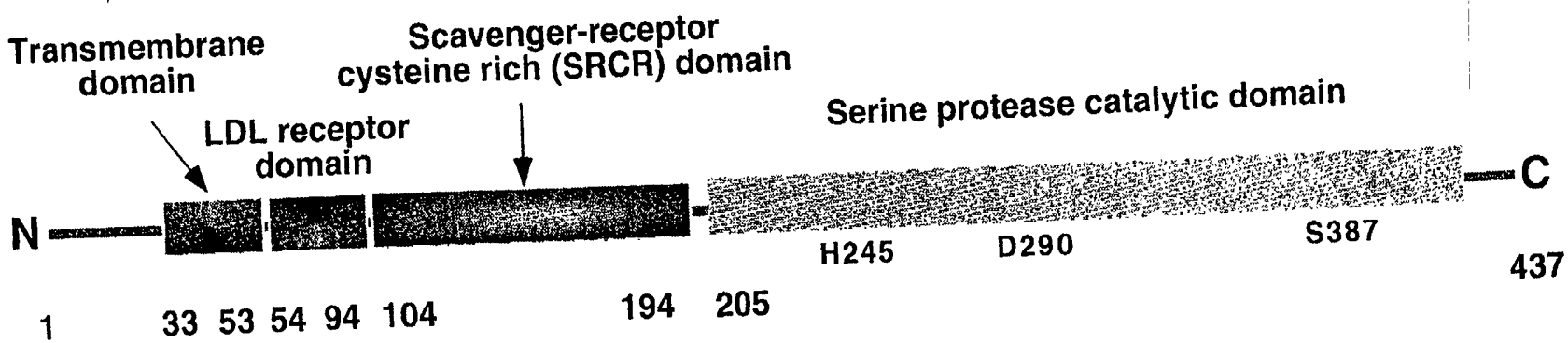

FIGURE 1

T02020 T6T9460

SPLICE VARIANT AND DOMAIN ORGANIZATION OF MTSP4

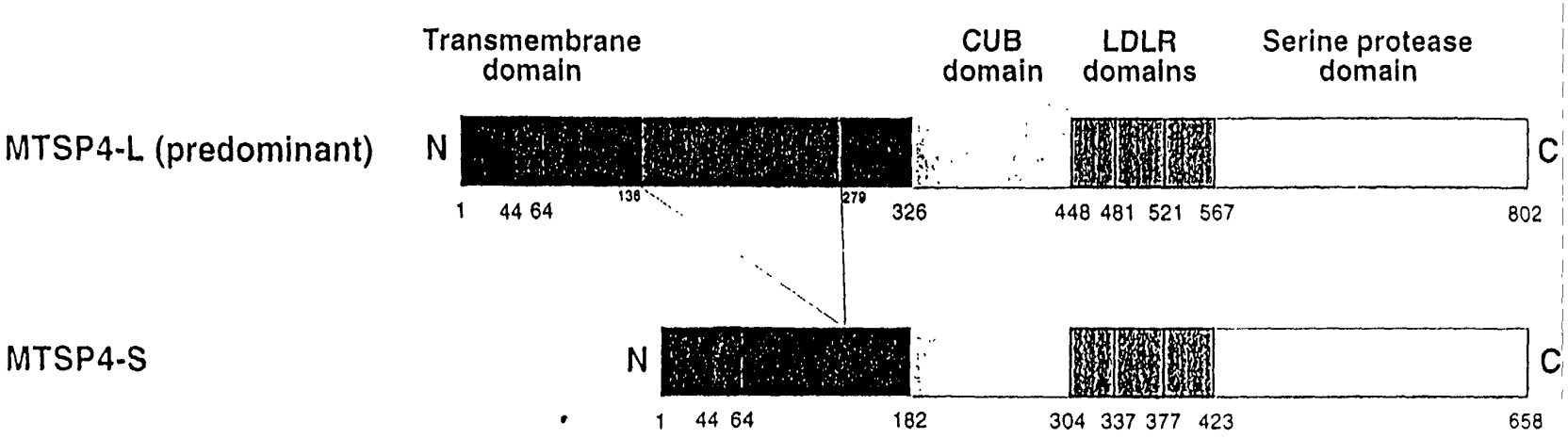

FIGURE 2

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DOMAIN ORGANIZATION OF HUMAN MTSP6

Transmembrane domain

LDL Receptor Class a domain

Scavenger receptor Cys-rich domain

Trypsin-like Serine protease domain

FIGURE 3

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                                                ▽
MTSP3     194 LACGKS----------------LKTPRVVGGEEASVDSWPWQVSIQYDKQHVCGGSILD 236
                                              205
MTSP4-S   396 PQCDGRPDCRDGSDEEHCECGLQGPSSRIVGGAVSSEGEWPWQASLQVRGRHICGGALIA 455
                                              424
MTSP4-L   540 PQCDGRPDCRDGSDEEHCECGLQGPSSRIVGGAVSSEGEWPWQASLQVRGRHICGGALIA 599
                                              568
MTSP6     205 TACGHR----------------RGYSSRIVGGNMSLLSQWPWQASLQFQGYHLCGGSVIT 248
                                              217 +

MTSP3     237 PHWVLTAAHCFRKHTDVFN--WKVRAGSDKLGS----FPSLAVAKIIIIEFNPMYPKDND 290
MTSP4-S   456 DRWVITAAHCFQEDSMASTVLWTVFLGKVWQNSRWPGEVSFKVSRLLLHPYHEEDSHDYD 515
MTSP4-L   600 DRWVITAAHCFQEDSMASTVLWTVFLGKVWQNSRWPGEVSFKVSRLLLHPYHEEDSHDYD 659
MTSP6     249 PLWIITAAHCVYDLYLPKS--WTIQVGLVSLLD--NPAPSHLVEKIVYHSKYKPKRLGND 304

MTSP3     291 IALMKLQFPLTFSGTVRPICLPFFDEELTPATPLWIIGWGFTKQNGGKMSDILLQASVQV 350
                                    *
MTSP4-S   516 VALLQLDHPVVRSAAVRPVCLPARSHFFEPGLHCWITGWGALRE-GGPISNALQKVDVQL 574
                                    *
MTSP4-L   660 VALLQLDHPVVRSAAVRPVCLPARSHFFEPGLHCWITGWGALRE-GGPISNALQKVDVQL 718
                                    *
MTSP6     305 IALMKLAGPLTFNEMIQPVCLPNSEENFPDGKVCWTSGWGATED-GGDASPVLNHAAVPL 363
                                    *

MTSP3     351 IDSTRCNADDAYQGEVTEKMMCAGIPEGGVDTCQGDSGGPLMYQSDQ--WHVVGIVSWGY 408
MTSP4-S   575 IPQDLCS--EVYRYQVTPRMLCAGYRKGKKDACQGDSGGPLVCKALSGRWFLAGLVSWGL 632
MTSP4-L   719 IPQDLCS--EVYRYQVTPRMLCAGYRKGKKDACQGDSGGPLVCKALSGRWFLAGLVSWGL 776
MTSP6     364 ISNKICNHRDVYGGIISPSMLCAGYLTGGVDSCQGDSGGPLVCQERR-LWKLVGATSFGI 422

MTSP3     409 GCGGPSTPGVYTKVSAYLNWIYNVWKAEL   437
MTSP4-S   633 GCGRPNYFGVYTRITGVISWIQQVVT      658
MTSP4-L   777 GCGRPNYFGVYTRITGVISWIQQVVT      802
MTSP6     423 GCAEVNKPGVYTRVTSFLDWIHEQMERDLKT 453
```

▽ cleavage site

\+ potential glycosylation site

* unpaired cysteine

FIGURE 4